

RESULT 1

A38084

galactose oxidase (EC 1.1.3.9) precursor [validated] - fungus (Cladobotryum dendroides)

C;Species: Cladobotryum dendroides

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C;Accession: A38084

R;McPherson, M.J.; Ogel, Z.B.; Stevens, C.; Yadav, K.D.S.; Keen, J.N.; Knowles, P.F.

J. Biol. Chem. 267, 8146-8152, 1992

A;Title: Galactose oxidase of Dactylium dendroides. Gene cloning and sequence analysis.

A;Reference number: A38084; MUID:92235025; PMID:1569070

A;Accession: A38084

A;Molecule type: DNA

A;Residues: 1-728 <MCP>

A;Cross-references: GB:M86819

A;Note: it is uncertain whether Met-1 or Met-49 is the initiator

A;Note: parts of this sequence, including the amino end of the mature protein, were confirmed by protein sequencing

R;Ito, N.; Phillips, S.E.V.; Stevens, C.; Ogel, Z.B.; McPherson, M.J.; Keen, J.N.; Yadav, K.D.S.; Knowles, P.F.

Nature 350, 87-90, 1991

A;Title: Novel thioether bond revealed by a 1.7 angstrom crystal structure of galactose oxidase.

A;Reference number: A48244; MUID:91163641; PMID:2002850

A;Contents: annotation

R;Ito, N.; Phillips, S.E.V.; Knowles, P.F.

submitted to the Brookhaven Protein Data Bank, September 1993

A;Reference number: A51740; PDB:1GOF

A;Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 90-728

R;Ito, N.; Phillips, S.E.V.; Knowles, P.F.

submitted to the Brookhaven Protein Data Bank, September 1993

A;Reference number: A51741; PDB:1GOG

A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 90-728

R;Ito, N.; Phillips, S.E.V.; Knowles, P.F.

submitted to the Brookhaven Protein Data Bank, September 1993

A;Reference number: A51742; PDB:1GOH

A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 90-728

C;Genetics:

A;Gene: gaoA

C;Superfamily: Cladobotryum dendroides galactose oxidase

C;Keywords: disulfide bond; metal binding; oxidoreductase

F;1-64/Domain: signal sequence #status predicted <SIG>

F;65-89/Domain: propeptide #status predicted <PRO>

F;90-728/Product: galactose oxidase #status experimental <MAT>

F;107-116,604-607/Disulfide bonds: #status experimental

F;317-361/Cross-link: cysteinyltyrosine (Cys-Tyr) #status experimental

F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental

F;419/Binding site: substrate (Arg) #status predicted

Query Match 99.9%; Score 3420; DB 1; Length 728;

Best Local Similarity 99.8%; Pred. No. 5.7e-206;

Matches 638; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYGANGDPKPPHTYTIDMK 60

|||||

Db 90 ASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYGANGDPKPPHTYTIDMK 149
 Qy 61 TTQNVNGLSMLPRQDGNQNGWIGRHEVYLSSDGTNWGSPVASGSWFADSTTKYSNFETRP 120
 |||||
 Db 150 TTQNVNGLSMLPRQDGNQNGWIGRHEVYLSSDGTNWGSPVASGSWFADSTTKYSNFETRP 209
 Qy 121 ARYVRLVAITEANGQPWTSIAEINVQASSYTAPQPGLGRWGPTIDLPIVPAAAAIEPTS 180
 |||||
 Db 210 ARYVRLVAITEANGQPWTSIAEINVQASSYTAPQPGLGRWGPTIDLPIVPAAAAIEPTS 269
 Qy 181 GRVLMWSSYRNDAFGGSPGGITLTSSWDPSTGIVSDRTVTVTKHDMFCPGISMDGNGQIV 240
 |||||
 Db 270 GRVLMWSSYRNDAFGGSPGGITLTSSWDPSTGIVSDRTVTVTKHDMFCPGISMDGNGQIV 329
 Qy 241 VTGGNDAKKTSLYDSSSDSWIPGPDQVARGYQSSATMSDGRVFTIGGSWSGGVFEKNGE 300
 |||||
 Db 330 VTGGNDAKKTSLYDSSSDSWIPGPDQVARGYQSSATMSDGRVFTIGGSWSGGVFEKNGE 389
 Qy 301 VYSPSSKTWTSLPNAKVNPMILTADKQGLYRSDNHAWLFGWKKGSVFQAGPSTAMNWWYTS 360
 |||||
 Db 390 VYSPSSKTWTSLPNAKVNPMILTADKQGLYRSDNHAWLFGWKKGSVFQAGPSTAMNWWYTS 449
 Qy 361 GSGDVKSSAGKRQSNRGVAPDAMCGNAVMYDAVKGKILTFGGSPDYQSDATNAHIITLG 420
 |||||
 Db 450 GSGDVKSSAGKRQSNRGVAPDAMCGNAVMYDAVKGKILTFGGSPDYQSDATNAHIITLG 509
 Qy 421 EPGTSPNTVFASNGLYFARTFHTSVVLPDGSTFITGGQRRGIPFEDSTPVFTPEIYVPEQ 480
 |||||
 Db 510 EPGTSPNTVFASNGLYFARTFHTSVVLPDGSTFITGGQRRGIPFEDSTPVFTPEIYVPEQ 569
 Qy 481 DTFYKQNPNSIVRVYHSISLLLPDGRVFNGGGGLCGDCTTNHFDAQIFTPNYLYNSDGNL 540
 |||||
 Db 570 DTFYKQNPNSIVRVYHSISLLLPDGRVFNGGGGLCGDCTTNHFDAQIFTPNYLYNSDGNL 629
 Qy 541 ATRPKITRTSTQSVKVGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGGN 600
 |||||
 Db 630 ATRPKITRTSTQSVKVGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGGN 689
 Qy 601 SYSFQVPSDSGVALPGYWMLFVMNSAGVPSVASTIRVTQ 639
 |||||
 Db 690 SYSFQVPSDSGVALPGYWMLFVMNSAGVPSVASTIRVTQ 728

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3420	99.9	639	4	US-09-782-906-2	Sequence 2, Appli
2	3401	99.3	639	4	US-09-782-906-3	Sequence 3, Appli
3	3391	99.0	639	4	US-09-782-906-4	Sequence 4, Appli
4	3390	99.0	639	4	US-09-782-906-5	Sequence 5, Appli
5	2207	64.4	679	3	US-09-257-536-2	Sequence 2, Appli
6	2207	64.4	679	3	US-09-512-230-2	Sequence 2, Appli
7	194	5.7	2736	4	US-09-252-991A-30227	Sequence 30227, A
8	170.5	5.0	1216	4	US-09-134-000C-5130	Sequence 5130, Ap
9	161	4.7	1752	4	US-09-865-621A-2	Sequence 2, Appli
10	150	4.4	1146	4	US-09-198-452A-580	Sequence 580, App
11	150	4.4	1749	4	US-09-640-419C-28	Sequence 28, Appl
12	143.5	4.2	3892	4	US-09-328-352-5503	Sequence 5503, Ap
13	137.5	4.0	642	4	US-09-337-307A-3	Sequence 3, Appli
14	137.5	4.0	642	4	US-09-337-307A-4	Sequence 4, Appli

** same mutation*

6498026

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1730	50.5	716	3	Q870R5	Q870r5 neurospora
2	452.5	13.2	779	2	Q938A2	Q938a2 stigmatella
3	416.5	12.2	526	2	Q53679	Q53679 stigmatella
4	414.5	12.1	757	16	Q82I66	Q82i66 streptomyce
5	337.5	9.9	645	16	Q9RDB4	Q9rdb4 streptomyce
6	300.5	8.8	656	16	Q81DE5	Q81de5 bacillus ce
7	299.5	8.7	645	16	Q82CX0	Q82cx0 streptomyce
8	298.5	8.7	615	10	Q9FYG4	Q9fyg4 arabidopsis
9	295	8.6	594	10	Q8RY19	Q8ry19 arabidopsis

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3420	99.9	680	1	GAOA_DACDE	Q01745 dactylium d
2	233	6.8	647	1	NANH_MICVI	Q02834 micromonosp
3	209	6.1	1014	1	NANH_CLOSE	P29767 clostridium
4	164	4.8	1723	1	KA93_HUMAN	Q9upq9 homo sapien
5	162	4.7	725	1	YA33_SULSO	Q97z97 sulfolobus
6	149	4.4	1723	1	PM20_CHLPN	Q9z812 chlamydia p
7	142.5	4.2	1902	1	P2P_LACPA	Q02470 lactobacill
8	141.5	4.1	751	1	KHL1_MOUSE	Q9ji74 mus musculu
9	141.5	4.1	959	1	N100_YEAST	Q02629 saccharomyc
10	140.5	4.1	827	1	XANP_XANS2	Q60106 xanthomonas
11	138.5	4.0	748	1	KHL1_HUMAN	Q9nr64 homo sapien
12	137	4.0	1356	1	HET1_PODAN	Q00808 podospora a
13	137	4.0	1656	1	OMPB_RICJA	O06653 r outer mem
14	136	4.0	1286	1	AIDA_ECOLI	Q03155 escherichia
15	135.5	4.0	916	1	SCRB_LIMPO	Q25386 limulus pol
16	135	3.9	2432	1	Y43R_IRV6	P18305 chilo iride
17	132	3.9	1147	1	TEA1_SCHPO	P87061 schizosacch
18	132	3.9	2003	1	YDBA_ECOLI	P33666 escherichia
19	131.5	3.8	1902	1	P2P_LALCL	P15293 lactococcus